

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/600,751A
Source: 1 Fw1,6
Date Processed by STIC: 1/24/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/24/2006

PATENT APPLICATION: US/10/600,751A

TIME: 15:57:14

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\01242006\J600751A.raw

4 <110> APPLICANT: BLEDSOE, RANDY K
 5 LAMBERT, MILLARD H
 6 MONTANA, VALERIE G
 7 STEWART, EUGENE L
 8 XU, H. ERIC
 10 <120> TITLE OF INVENTION: METHOD FOR IDENTIFYING A GLUCOCORTICOID
 11 RECEPTOR MODULATOR USING THE STRUCTURE OF A GLUCOCORTICOID
 12 RECEPTOR LIGAND BINDING DOMAIN (TITLE AS AMENDED)
 15 <130> FILE REFERENCE: PU4803 US
 17 <140> CURRENT APPLICATION NUMBER: US 10/600,751A
 18 <141> CURRENT FILING DATE: 2003-06-20
 20 <150> PRIOR APPLICATION NUMBER: US 60/390,610
 21 <151> PRIOR FILING DATE: 2002-06-21
 23 <160> NUMBER OF SEQ ID NOS: 14
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2334
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo Sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)...(2334)
 36 <400> SEQUENCE: 1
 37 atg gac tcc aaa gaa tca tta act cct ggt aga gaa gaa aac ccc agc 48
 38 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 39 1 5 10 15
 41 agt gtg ctt gct cag gag agg gga gat gtg atg gac ttc tat aaa acc 96
 42 Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 43 20 25 30
 45 cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg 144
 46 Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 47 35 40 45
 49 gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat 192
 50 Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 51 50 55 60
 53 ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa 240
 54 Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 55 65 70 75 80
 57 gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa 288
 58 Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 59 85 90 95
 61 gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt 336
 62 Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu

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63	100	105	110	
65	tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac	384		
66	Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn			
67	115	120	125	
69	ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc	432		
70	Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser			
71	130	135	140	
73	act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac	480		
74	Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His			
75	145	150	155	160
77	tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc	528		
78	Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr			
79	165	170	175	
81	aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac	576		
82	Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp			
83	180	185	190	
85	att ttg cag gat ttg gag ttt tct tct ggg tcc cca ggt aaa gag acg	624		
86	Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr			
87	195	200	205	
89	aat gag agt cct tgg aga tca gac ctg ttg ata gat gaa aac tgt ttg	672		
90	Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu			
91	210	215	220	
93	ctt tct cct ctg gcg gga gaa gac gat tca ttc ctt ttg gaa gga aac	720		
94	Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn			
95	225	230	235	240
97	tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa	768		
98	Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys			
99	245	250	255	
101	att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca	816		
102	Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr			
103	260	265	270	
105	ctg ccc caa gtg aaa aca gaa aaa gaa gat ttc atc gaa ctc tgc acc	864		
106	Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr			
107	275	280	285	
109	cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca	912		
110	Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala			
111	290	295	300	
113	agc ttt cct gga gca aat ata att ggt aat aaa atg tct gcc att tct	960		
114	Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser			
115	305	310	315	320
117	gtt cat ggt gtg agt acc tct gga gga cag atg tac cac tat gac atg	1008		
118	Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met			
119	325	330	335	
121	aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat	1056		
122	Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn			
123	340	345	350	
125	gtc att cca cca att ccc gtt ggt tcc gaa aat tgg aat agg tgc caa	1104		
126	Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln			
127	355	360	365	

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129 gga tct gga gat gac aac ttg act tct ctg ggg act ctg aac ttc cct 1152
130 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
131 370 375 380
133 ggt cga aca gtt ttt tct aat ggc tat tca agc ccc agc atg aga cca 1200
134 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
135 385 390 395 400
137 gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca 1248
138 Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
139 405 410 415
141 cct ccc aaa ctg tgc ctg gtg tgc tct gat gaa gct tca gga tgt cat 1296
142 Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
143 420 425 430
145 tat gga gtc tta act tgt gga agc tgt aaa gtt ttc ttc aaa aga gca 1344
146 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
147 435 440 445
149 gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc 1392
150 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
151 450 455 460
153 atc gat aaa att cga aga aaa aac tgc cca gca tgc cgc tat cga aaa 1440
154 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
155 465 470 475 480
157 tgt ctt cag gct gga atg aac ctg gaa gct cga aaa aca aag aaa aaa 1488
158 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
159 485 490 495
161 ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct 1536
162 Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
163 500 505 510
165 gaa aat cct ggt aac aaa aca ata gtt cct gca acg tta cca caa ctg 1584
166 Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
167 515 520 525
169 acc cct acc ctg gtg tca ctg ttg gag gtt att gaa cct gaa gtg tta 1632
170 Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
171 530 535 540
173 tat gca gga tat gat agc tct gtt cca gac tca act tgg agg atc atg 1680
174 Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
175 545 550 555 560
177 act acg ctg aac atg tta gga ggg cgg caa gtg att gca gca gtg aaa 1728
178 Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
179 565 570 575
181 tgg gca aag gca ata cca ggt ttc agg aac tta cac ctg gat gac caa 1776
182 Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
183 580 585 590
185 atg acc cta ctg cag tac tcc tgg atg ttt ctt atg gca ttt gct ctg 1824
186 Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu
187 595 600 605
189 ggg tgg aga tca tat aga caa tca agt gca aac ctg ctg tgt ttt gct 1872
190 Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
191 610 615 620
193 cct gat ctg att att aat gag cag aga atg act cta ccc tgc atg tac 1920

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194 Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
195 625                      630                      635                      640
197 gac caa tgt aaa cac atg ctg tat gtt tcc tct gag tta cac agg ctt 1968
198 Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
199                      645                      650                      655
201 cag gta tct tat gaa gag tat ctc tgt atg aaa acc tta ctg ctt ctc 2016
202 Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
203                      660                      665                      670
205 tct tca gtt cct aag gac ggt ctg aag agc caa gag cta ttt gat gaa 2064
206 Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
207                      675                      680                      685
209 att aga atg acc tac atc aaa gag cta gga aaa gcc att gtc aag agg 2112
210 Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
211                      690                      695                      700
213 gaa gga aac tcc agc cag aac tgg cag cgg ttt tat caa ctg aca aaa 2160
214 Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
215 705                      710                      715                      720
217 ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc 2208
218 Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
219                      725                      730                      735
221 ttc caa aca ttt ttg gat aag acc atg agt att gaa ttc ccc gag atg 2256
222 Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
223                      740                      745                      750
225 tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat 2304
226 Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
227                      755                      760                      765
229 atc aaa aaa ctt ctg ttt cat caa aag tga 2334
230 Ile Lys Lys Leu Leu Phe His Gln Lys *
231 770                      775
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 777
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo Sapiens
239 <400> SEQUENCE: 2
240 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
241 1                      5                      10                      15
242 Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
243                      20                      25                      30
244 Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
245                      35                      40                      45
246 Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
247                      50                      55                      60
248 Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
249 65                      70                      75                      80
250 Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
251                      85                      90                      95
252 Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
253                      100                     105                     110
254 Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn

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```

255          115          120          125
256 Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
257          130          135          140
258 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
259 145          150          155          160
260 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
261          165          170          175
262 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
263          180          185          190
264 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
265          195          200          205
266 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
267          210          215          220
268 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
269 225          230          235          240
270 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
271          245          250          255
272 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
273          260          265          270
274 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
275          275          280          285
276 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
277          290          295          300
278 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
279 305          310          315          320
280 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
281          325          330          335
282 Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
283          340          345          350
284 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
285          355          360          365
286 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
287          370          375          380
288 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
289 385          390          395          400
290 Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
291          405          410          415
292 Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
293          420          425          430
294 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
295          435          440          445
296 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
297          450          455          460
298 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
299 465          470          475          480
300 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
301          485          490          495
302 Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
303          500          505          510

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/600,751A

DATE: 01/24/2006
TIME: 15:57:16

Input Set : A:\SEQLIST.TXT
Output Set: N:\CRF4\01242006\J600751A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 2,3

VERIFICATION SUMMARY

DATE: 01/24/2006

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L:916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0